(a) isolating a cytoplasmic fraction which includes mitochondria from the embryonic cell according to the method of claim 16; and

(b) comparing the number of mitochondrial genomes in the fraction with a nucleotide sequence, polymorphism or mutation, with the number of genomes without the nucleotide sequence, polymorphism or mutation in the fraction.

28. A method according to claim 27 wherein the nucleotide sequence, polymorphism or mutation of the mitochondrial genome is one which causes, or is suspected of causing, or is associated with, a disease or dysfunction in the embryonic cell, or in progeny descended from the cell.

29. A method according to claim 28 wherein the nucleotide sequence, polymorphism or mutation is shown in Table 1.